SPECIFICATION AMENDMENTS

Please amend the specification as indicated on the marked-up versions of pages 7, 8, and 9 which follow.

diminished 11-Kb *Eco*RI band as well as one nongermline and (→) that identified a monoclonal pattern of Tcrβ gene arrangement. Furthermore, there was a diminution of the 8.0-Kb *Hind*III digest that reflects a monoclonal Tcrβ pattern of gene rearrangement as well. This Southern blot pattern indicates that one Tcrβ allele in the leukemic clone rearranged to Cβ1, whereas the other allele rearranged to Cβ2. Digests of patient DNA obtained in remission following ^{90}Y anti-Tac therapy did not reveal the two non-germline brands, thus confirming the elimination of the circulating monoclonal leukemic cell population. In the schematic diagram of the germline arrangement of the Tcrβ gene, we indicate the locations of the *Eco*RI (E) and *Hind*III (H) restriction endonuclease sites as well as the Cβ regions recognized by the cDNA probe used.

~~Fig. 5. Southern blot analysis of HTLV-I proviral integration in *Pst*I and *Eco*RI digests of DNA obtained from the peripheral blood mononuclear cells of Patient 7. (A) There are no *Eco*RI restriction sites within the HTLV-I genome. Therefore the generation of a band identifying a restriction-length fragment containing HTLV-1 depends on the recognition of *Eco*RI sites in host DNA adjacent to viral integration. Clonal integration of the complete virus is indicated by a band in an *Eco*RI digest that is larger than 9 Kb, the size of viral genome. The presence of a single band (→) demonstrable in the *Eco*RI digest of mononuclear cell DNA for Patient 7 during active disease demonstrates monoclonal viral integration into the leukemic cell DNA of the patient. This band was no longer evident on *Eco*RI digests obtained during ^{90}Y anti-Tac induced complete remission. (B) There are multiple *Pst*I restriction sites within the complete HTLV-1 genome that on digestion of both polyclonally and monoclonally integrated HTLV-1 yield three bands of 1.2, 1.8, and 2.5 Kb. In digests of Patient 7 mononuclear cell DNA obtained~~

~~during active disease there are two additional bands (→) indicating monoclonal viral integration that identify one *Pst*I site within HTLV-1 and another in host DNA adjacent to the virus. This pattern is the hallmark of the presence of clonally integrated HTLV-1 in the leukemic cell DNA. No bands reflecting residual HTLV-1 were demonstrable in the *Pst*I digest of the DNA of circulating cells obtained from the patient on day 818 following initiation of therapy, supporting the view that this patient was in a complete remission. Each lane contains 10 μg of genomic DNA. Ethidium bromide staining confirmed that equivalent quantities of genomic DNA were present in each lane. A schematic diagram of the virus indicating *Eco*RI and *Pst*I restriction endonuclease sites is shown below.~~

Fig. ~~6.~~ 5. CAT scan of thorax of Patient 4 before treatment (top) and after two cycles of ^{90}Y anti-Tac therapy (bottom). There was a marked reduction in the size of the axillary lymph nodes in the scan obtained during the period when the patient was in an ^{90}Y anti-Tac therapy-induced partial remission.

Fig. ~~7.~~ 6. ^{111}In anti-Tac imaging studies of Patient 1 prior to treatment and at the time of the fourth treatment with ^{90}Y anti-Tac when the patient was in a complete remission. Prior to therapy ^{111}In anti-Tac was deposited in sites of malignant T-cell infiltration of the skin of the hands, whereas no such deposition was evident at the time of the fourth study confirming the complete remission.

~~Fig. 8. ^{111}In anti-Tac anterior whole body scans from Patient 4 obtained at 48 hours post-tracer administration. Left panel shows accumulation in involved axillary, cervical, inguinal, and hilar nodes in the images obtained at the time of the initial therapeutic infusion. The patient received 5 mCi of ^{111}In and 10 mCi~~

~~of ^{90}Y anti-Tac with a total of 10 mg of antibody. The right panel was obtained 6 weeks after the patient's first therapy. The imaging dose was identical to the first dose. The ^{111}In anti-Tac study revealed a marked decrease in tumor size and more prolonged circulation of the tracer labeled antibody, which was associated with the decreased tumor burden.~~

Fig. ~~9.~~ 7.(A) Effect of ^{90}Y anti-Tac therapy on the absolute number of Tac-expressing ATL leukemic and normal T cells/mm^3 of Patient 7. ^{90}Y anti-Tac monoclonal antibody was administered i.v. to the patient at the doses and on the days indicated by the arrows (→). The patient initially had 27,875 circulating Tac-expressing malignant cells/mm^3(-·) The patient received 50 mCi of ^{90}Y anti-Tac during the first 410 days of therapy in divided doses. By day 300 following initiation of therapy, the patient had undergone a complete remission that has been maintained for the over 800-day period of observation. There was an initial modest reduction in the number of normal T cells (o-) (normal T cells are $CD7^+CD25^-$). However, the number of these normal T cells subsequently returned to pretreatment levels during the remaining period when the patient was in a sustained complete remission. (B) Effect of ^{90}Y anti-Tac therapy on the serum concentration of sIL-2Rα of the same patient. The serum sIL-2Rα level of the patient prior to therapy was 2,938 units/ml. The concentration sIL-2Rα returned to normal or below normal levels following therapy confirming the complete remission.

Fig. ~~10.~~ 8.A Kaplan-Meier plot (1958 *J. Am. Stat. Assoc.* 53:457) of event-free survival (surviving patients without progressive disease) comparing patients treated with unmodified anti-Tac (---) with those receiving ^{90}Y anti-Tac (—).